



FB

## RAW SEQUENCE LISTING ERROR REPORT

5000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/857,000  
Source: PC709  
Date Processed by STIC: 4/8/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

PCT09

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/857,000

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☒ Variable Length      Sequence(s) 940 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☒ Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



**Does Not Comply** PCT09  
**Corrected Diskette Needed**

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/857,000

DATE: 04/08/2002

TIME: 13:59:24

Input Set : A:\Breese.txt

Output Set: N:\CRF3\04082002\I857000.raw

4 <110> APPLICANT: Philippe, CLAIR  
5 Michel, KACZOREK  
6 Jamal, TEMSAMANI  
8 <120> TITLE OF INVENTION: Peptides carrying substances across the blood brain barrier  
10 <130> FILE REFERENCE: 3373PCT/US  
12 <140> CURRENT APPLICATION NUMBER: US 09/857,000  
C--> 13 <141> CURRENT FILING DATE: 2001-09-07  
15 <150> PRIOR APPLICATION NUMBER: FR98/15074  
16 <151> PRIOR FILING DATE: 1998-11-30  
18 <150> PRIOR APPLICATION NUMBER: PCT/FR99/02938  
19 <151> PRIOR FILING DATE: 1999-11-26  
21 <160> NUMBER OF SEQ ID NOS: 13  
22 <170> SOFTWARE: PatentIn version 3.1

**ERRORED SEQUENCES**

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

167 <210> SEQ ID NO: 9  
168 <211> LENGTH: 18  
169 <212> TYPE: PRT  
170 <213> ORGANISM: unidentified — invalid response, see error summary sheet, item 10  
W--> 171 <220> FEATURE:  
172 <221> NAME/KEY: MISC\_FEATURE  
173 <222> LOCATION: (1)..(1)  
174 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries  
W--> 176 <220> FEATURE:  
177 <221> NAME/KEY: MISC\_FEATURE  
178 <222> LOCATION: (2)..(2)  
179 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 182 <220> FEATURE:  
183 <221> NAME/KEY: MISC\_FEATURE  
184 <222> LOCATION: (3)..(3)  
185 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 187 <220> FEATURE:  
188 <221> NAME/KEY: MISC\_FEATURE  
189 <222> LOCATION: (4)..(4)  
190 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an

amino acid for which the side chain carries

W--> 192 <220> FEATURE:

193 <221> NAME/KEY: MISC\_FEATURE

194 <222> LOCATION: (5)..(5)

195 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 197 <220> FEATURE:

198 <221> NAME/KEY: MISC\_FEATURE

## RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/857,000

TIME: 13:59:25

Input Set : A:\Breese.txt

Output Set : N:\CRF3\04082002\I857000.raw

199 <222> LOCATION: (6)..(6)  
200 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 202 <220> FEATURE:  
203 <221> NAME/KEY: MISC\_FEATURE  
204 <222> LOCATION: (7)..(7)  
205 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 207 <220> FEATURE:  
208 <221> NAME/KEY: MISC\_FEATURE  
209 <222> LOCATION: (8)..(8)  
210 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 212 <220> FEATURE:  
213 <221> NAME/KEY: MISC\_FEATURE  
214 <222> LOCATION: (9)..(9)  
215 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries  
W--> 217 <220> FEATURE:  
218 <221> NAME/KEY: MISC\_FEATURE  
219 <222> LOCATION: (10)..(10)  
220 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries  
W--> 222 <220> FEATURE:  
223 <221> NAME/KEY: MISC\_FEATURE  
224 <222> LOCATION: (11)..(11)  
225 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries  
W--> 226 <220> FEATURE:  
227 <221> NAME/KEY: MISC\_FEATURE  
228 <222> LOCATION: (12)..(12)  
229 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 231 <220> FEATURE:  
232 <221> NAME/KEY: MISC\_FEATURE  
233 <222> LOCATION: (13)..(13)  
234 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 236 <220> FEATURE:  
237 <221> NAME/KEY: MISC\_FEATURE  
238 <222> LOCATION: (14)..(14)  
239 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 241 <220> FEATURE:

242 <221> NAME/KEY: MISC\_FEATURE  
243 <222> LOCATION: (15)..(15)  
244 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 246 <220> FEATURE:  
247 <221> NAME/KEY: MISC\_FEATURE  
248 <222> LOCATION: (16)..(16)  
249 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 251 <220> FEATURE:  
252 <221> NAME/KEY: MISC\_FEATURE  
253 <222> LOCATION: (17)..(17)  
254 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid  
W--> 256 <220> FEATURE:  
257 <221> NAME/KEY: MISC\_FEATURE  
258 <222> LOCATION: (18)..(18)

## RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/857,000

TIME: 13:59:25

Input Set : A:\Breese.txt

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259 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

W--> 261 <220> FEATURE:

262 <221> NAME/KEY: PEPTIDE

263 <222> LOCATION: (1)..(18)

264 <223> OTHER INFORMATION: Peptide of formula (II)

W--> 265 <400> SEQUENCE: 9

E--> 267 Baa Xaa Xaa Baa Xaa Xaa Xaa Xaa Baa Baa Baa Xaa Xaa Xaa Xaa

268 1 5 10 15

Baa is not a valid amino acid designator

E--> 271 Xaa Baa

274 <210> SEQ ID NO: 10

275 <211> LENGTH: 17

276 <212> TYPE: PRT

277 <213> ORGANISM: unidentified

- invalid response (same error)

W--> 278 <220> FEATURE:

279 <221> NAME/KEY: MISC\_FEATURE

280 <222> LOCATION: (1)..(1)

281 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

W--> 283 <220> FEATURE:

284 <221> NAME/KEY: MISC\_FEATURE

285 <222> LOCATION: (2)..(2)

286 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 288 <220> FEATURE:

289 <221> NAME/KEY: MISC\_FEATURE

290 <222> LOCATION: (3)..(3)

291 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 293 <220> FEATURE:

294 <221> NAME/KEY: MISC\_FEATURE

295 <222> LOCATION: (4)..(4)

296 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 298 <220> FEATURE:

299 <221> NAME/KEY: MISC\_FEATURE

300 <222> LOCATION: (5)..(5)

301 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

W--> 303 <220> FEATURE:

304 <221> NAME/KEY: MISC\_FEATURE

305 <222> LOCATION: (6)..(6)

306 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 308 <220> FEATURE:

309 <221> NAME/KEY: MISC\_FEATURE

310 <222> LOCATION: (7)..(7)

311 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 313 <220> FEATURE:

314 <221> NAME/KEY: MISC\_FEATURE

315 <222> LOCATION: (8)..(8)

316 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

W--> 320 <220> FEATURE:

321 <221> NAME/KEY: MISC\_FEATURE

322 <222> LOCATION: (9)..(9)

323 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries



## RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/857,000

TIME: 13:59:25

Input Set : A:\Breese.txt

Output Set: N:\CRF3\04082002\I857000.raw

## W--&gt; 325 &lt;220&gt; FEATURE:

326 &lt;221&gt; NAME/KEY: MISC\_FEATURE

327 &lt;222&gt; LOCATION: (10)..(10)

328 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

## W--&gt; 330 &lt;220&gt; FEATURE:

331 &lt;221&gt; NAME/KEY: MISC\_FEATURE

332 &lt;222&gt; LOCATION: (11)..(11)

333 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

## W--&gt; 335 &lt;220&gt; FEATURE:

336 &lt;221&gt; NAME/KEY: MISC\_FEATURE

337 &lt;222&gt; LOCATION: (12)..(12)

338 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

## W--&gt; 340 &lt;220&gt; FEATURE:

341 &lt;221&gt; NAME/KEY: MISC\_FEATURE

342 &lt;222&gt; LOCATION: (13)..(13)

343 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

## W--&gt; 345 &lt;220&gt; FEATURE:

346 &lt;221&gt; NAME/KEY: MISC\_FEATURE

347 &lt;222&gt; LOCATION: (14)..(14)

348 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

## W--&gt; 350 &lt;220&gt; FEATURE:

351 &lt;221&gt; NAME/KEY: MISC\_FEATURE

352 &lt;222&gt; LOCATION: (15)..(15)

353 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

## W--&gt; 355 &lt;220&gt; FEATURE:

356 &lt;221&gt; NAME/KEY: MISC\_FEATURE

357 &lt;222&gt; LOCATION: (16)..(16)

358 <223> OTHER INFORMATION: Groups X may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent a residue of aliphatic or aromatic amino acid

## W--&gt; 360 &lt;220&gt; FEATURE:

361 &lt;221&gt; NAME/KEY: MISC\_FEATURE

362 &lt;222&gt; LOCATION: (17)..(17)

363 <223> OTHER INFORMATION: Groups B may be identical or different, and represent a natural or non-natural amino acid, including amino acid with D configuration and represent an amino acid for which the side chain carries

## W--&gt; 364 &lt;220&gt; FEATURE:

365 &lt;221&gt; NAME/KEY: PEPTIDE

366 &lt;222&gt; LOCATION: (1)..(17)

367 &lt;223&gt; OTHER INFORMATION: Peptide of formula (III)

## W--&gt; 368 &lt;400&gt; SEQUENCE: 10

E--> 371 Baa Xaa Xaa Xaa Baa Xaa Xaa Xaa Baa Xaa Xaa Xaa Xaa Baa Baa Xaa  
 372 1 5 10 15  
 E--> 375 Baa

- error same

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,000

DATE: 04/08/2002

TIME: 13:59:26

Input Set : A:\Breese.txt

Output Set : N:\CRF3\04082002\I857000.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:29 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:47 M:283 W: Missing Blank Line separator, <220> field identifier  
L:51 M:283 W: Missing Blank Line separator, <400> field identifier  
L:61 M:283 W: Missing Blank Line separator, <220> field identifier  
L:65 M:283 W: Missing Blank Line separator, <400> field identifier  
L:79 M:283 W: Missing Blank Line separator, <220> field identifier  
L:83 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:283 W: Missing Blank Line separator, <220> field identifier  
L:101 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:283 W: Missing Blank Line separator, <220> field identifier  
L:119 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:283 W: Missing Blank Line separator, <220> field identifier  
L:137 M:283 W: Missing Blank Line separator, <400> field identifier  
L:161 M:283 W: Missing Blank Line separator, <400> field identifier  
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:171 M:283 W: Missing Blank Line separator, <220> field identifier  
L:226 M:283 W: Missing Blank Line separator, <220> field identifier  
L:265 M:283 W: Missing Blank Line separator, <400> field identifier  
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5  
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:271 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:278 M:283 W: Missing Blank Line separator, <220> field identifier  
L:364 M:283 W: Missing Blank Line separator, <220> field identifier  
L:368 M:283 W: Missing Blank Line separator, <400> field identifier  
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:371 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5  
L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:383 M:283 W: Missing Blank Line separator, <220> field identifier  
L:387 M:283 W: Missing Blank Line separator, <400> field identifier  
L:401 M:283 W: Missing Blank Line separator, <220> field identifier  
L:405 M:283 W: Missing Blank Line separator, <400> field identifier  
L:415 M:283 W: Missing Blank Line separator, <220> field identifier  
L:419 M:283 W: Missing Blank Line separator, <400> field identifier